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## RAW SEQUENCE LISTING

DATE: 10/30/2002

PATENT APPLICATION: US/10/032,221B

TIME: 15:08:29

Input Set.: A:\10\_032221.ST25.txt

Output Set: N:\CRF4\10302002\J032221B.raw

3 <110> APPLICANT: Kalluri, Raghuram  
 5 <120> TITLE OF INVENTION: ANTI-ANGIOGENIC PROTEINS AND FRAGMENTS AND METHODS OF USE  
 THEREOF

7 &lt;130&gt; FILE REFERENCE: 2312/2082B (formerly 1440.1027-016)

9 &lt;140&gt; CURRENT APPLICATION NUMBER: US 10/032,221B

10 &lt;141&gt; CURRENT FILING DATE: 2001-12-21

12 &lt;150&gt; PRIOR APPLICATION NUMBER: PCT/US01/00565

13 &lt;151&gt; PRIOR FILING DATE: 2001-01-08

15 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/625,191

16 &lt;151&gt; PRIOR FILING DATE: 2000-07-21

18 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/543,371

19 &lt;151&gt; PRIOR FILING DATE: 2000-04-04

21 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/479,118

22 &lt;151&gt; PRIOR FILING DATE: 2000-01-07

24 &lt;150&gt; PRIOR APPLICATION NUMBER: US 09/335,224

25 &lt;151&gt; PRIOR FILING DATE: 1999-06-17

27 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/126,175

28 &lt;151&gt; PRIOR FILING DATE: 1999-03-25

30 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/089,689

31 &lt;151&gt; PRIOR FILING DATE: 1998-06-17

33 &lt;160&gt; NUMBER OF SEQ ID NOS: 58

35 &lt;170&gt; SOFTWARE: PatentIn version 3.1

37 &lt;210&gt; SEQ ID NO: 1

38 &lt;211&gt; LENGTH: 690

39 &lt;212&gt; TYPE: DNA

40 &lt;213&gt; ORGANISM: Homo sapiens

42 &lt;220&gt; FEATURE:

43 &lt;221&gt; NAME/KEY: CDS

44 &lt;222&gt; LOCATION: (1)..(687)

45 &lt;223&gt; OTHER INFORMATION:

W--&gt; 47 &lt;400&gt; 1

48 tct gtt gat cac ggc ttc ctt gtg acc agg cat agt caa aca ata gat 48

49 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp

50 1 5 10 15

52 gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct 96

53 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser

54 20 25 30

56 ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc 144

57 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly

58 35 40 45

60 acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc 192

61 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe

62 50 55 60

64 tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg 240

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65 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
66 65          70          75          80
68 tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc      288
69 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
70          85          90          95
72 acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag      336
73 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
74          100          105          110
76 gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc cca      384
77 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
78          115          120          125
80 ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt gtg      432
81 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
82          130          135          140
84 atg cac acc agc gct ggt gca gaa ggc tct ggc caa gcc ctg gcg tcc      480
85 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
86 145          150          155          160
88 ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag tgt      528
89 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
90          165          170          175
92 cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt tgg      576
93 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
94          180          185          190
96 ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg tcc      624
97 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
98          195          200          205
100 acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa gtc      672
101 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
102          210          215          220
104 tgt atg aga aga aca taa      690
105 Cys Met Arg Arg Thr
106 225
109 <210> SEQ ID NO: 2
110 <211> LENGTH: 229
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapiens
114 <400> SEQUENCE: 2
116 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp
117 1          5          10          15
120 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
121          20          25          30
124 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
125          35          40          45
128 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
129          50          55          60
132 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
133 65          70          75          80
136 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
137          85          90          95

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Input Set : A:\10\_032221.ST25.txt

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140 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
141           100           105           110
144 Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
145           115           120           125
148 Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
149           130           135           140
152 Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
153 145           150           155           160
156 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
157           165           170           175
160 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
161           180           185           190
164 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
165           195           200           205
168 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
169           210           215           220

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172 Cys Met Arg Arg Thr

173 225

176 &lt;210&gt; SEQ ID NO: 3

177 &lt;211&gt; LENGTH: 27

178 &lt;212&gt; TYPE: DNA

179 &lt;213&gt; ORGANISM: Artificial sequence

181 &lt;220&gt; FEATURE:

182 &lt;223&gt; OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for Arresten

184 &lt;400&gt; SEQUENCE: 3

185 cgggatacctt ctgttgatca cggcttc

27

188 &lt;210&gt; SEQ ID NO: 4

189 &lt;211&gt; LENGTH: 27

190 &lt;212&gt; TYPE: DNA

191 &lt;213&gt; ORGANISM: Artificial sequence

193 &lt;220&gt; FEATURE:

194 &lt;223&gt; OTHER INFORMATION: pET22b(+) reverse oligonucleotide primer for Arresten

196 &lt;400&gt; SEQUENCE: 4

197 cccaagcttt gttctttctca tacagac

27

200 &lt;210&gt; SEQ ID NO: 5

201 &lt;211&gt; LENGTH: 684

202 &lt;212&gt; TYPE: DNA

203 &lt;213&gt; ORGANISM: Homo sapiens

205 &lt;220&gt; FEATURE:

206 &lt;221&gt; NAME/KEY: CDS

207 &lt;222&gt; LOCATION: (1)..(681)

208 &lt;223&gt; OTHER INFORMATION:

W--&gt; 210 &lt;400&gt; 5

211 gtc agc atc ggc tac ctc ctg gtg aag cac agc cag acg gac cag gag

48

212 Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu

213 1

5

10

15

215 ccc atg tgc ccg gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg

96

216 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu

217

20

25

30

## RAW SEQUENCE LISTING

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TIME: 15:08:29

Input Set : A:\10\_032221.ST25.txt

Output Set: N:\CRF4\10302002\J032221B.raw

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219 ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg      144
220 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
221      35      40      45
223 gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc      192
224 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
225      50      55      60
227 aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac      240
228 Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
229 65      70      75      80
231 tgg ctc tct acc act gcg ccg ctg ccc atg atg ccc gtg gcc gag gac      288
232 Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Pro Val Ala Glu Asp
233      85      90      95
235 gag atc aag ccc tac atc agc cgc tgt tct gtg tgt gag gcc ccg gcc      336
236 Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
237      100      105      110
239 atc gcc atc gcg gtc cac agt cag gat gtc tcc atc cca cac tgc cca      384
240 Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
241      115      120      125
243 gct ggg tgg cgg agt ttg tgg atc gga tat tcc ttc ctc atg cac acg      432
244 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
245      130      135      140
247 gcg gcg gga gac gaa ggc ggt ggc caa tca ctg gtg tca ccg ggc agc      480
248 Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
249 145      150      155      160
251 tgt cta gag gac ttc cgc gcc aca cca ttc atc gaa tgc aat gga ggc      528
252 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
253      165      170      175
255 cgc ggc acc tgc cac tac tac gcc aac aag tac agc ttc tgg ctg acc      576
256 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
257      180      185      190
259 acc att ccc gag cag agc ttc cag ggc tgc ccc tcc gcc gac acg ctc      624
260 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
261      195      200      205
263 aag gcc ggc ctc atc cgc aca cac atc agc cgc tgc cag gtg tgc atg      672
264 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
265      210      215      220
267 aag aac ctg tga      684
268 Lys Asn Leu
269 225
272 <210> SEQ ID NO: 6
273 <211> LENGTH: 227
274 <212> TYPE: PRT
275 <213> ORGANISM: Homo sapiens
277 <400> SEQUENCE: 6
279 Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu
280 1      5      10      15
283 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
284      20      25      30
287 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu

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Input Set : A:\10\_032221.ST25.txt

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288          35          40          45
291 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
292          50          55          60
295 Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr
296 65          70          75          80
299 Trp Leu Ser Thr Thr Ala Pro Leu Pro Met Met Pro Val Ala Glu Asp
300          85          90          95
303 Glu Ile Lys Pro Tyr Ile Ser Arg Cys Ser Val Cys Glu Ala Pro Ala
304          100          105          110
307 Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
308          115          120          125
311 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
312          130          135          140
315 Ala Ala Gly Asp Glu Gly Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
316 145          150          155          160
319 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
320          165          170          175
323 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
324          180          185          190
327 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
328          195          200          205
331 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
332          210          215          220
335 Lys Asn Leu
336 225

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339 &lt;210&gt; SEQ ID NO: 7

340 &lt;211&gt; LENGTH: 27

341 &lt;212&gt; TYPE: DNA

342 &lt;213&gt; ORGANISM: Artificial sequence

344 &lt;220&gt; FEATURE:

345 &lt;223&gt; OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for Canstatin

347 &lt;400&gt; SEQUENCE: 7

348 cgggatcctg tcagcatcgg ctacctc

27

351 &lt;210&gt; SEQ ID NO: 8

352 &lt;211&gt; LENGTH: 27

353 &lt;212&gt; TYPE: DNA

354 &lt;213&gt; ORGANISM: Artificial sequence

356 &lt;220&gt; FEATURE:

357 &lt;223&gt; OTHER INFORMATION: pET22b(+) reverse oligonucleotide primer for Canstatin

359 &lt;400&gt; SEQUENCE: 8

360 cccaagcttc aggtttctca tgcacac

27

363 &lt;210&gt; SEQ ID NO: 9

364 &lt;211&gt; LENGTH: 735

365 &lt;212&gt; TYPE: DNA

366 &lt;213&gt; ORGANISM: Homo sapiens

368 &lt;220&gt; FEATURE:

369 &lt;221&gt; NAME/KEY: CDS

370 &lt;222&gt; LOCATION: (1)..(732)

371 &lt;223&gt; OTHER INFORMATION:

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 10/30/2002  
PATENT APPLICATION:    US/10/032,221B      TIME: 15:08:30

Input Set : A:\10\_032221.ST25.txt  
Output Set: N:\CRF4\10302002\J032221B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 1,2,5,9,11,14

VERIFICATION SUMMARY

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TIME: 15:08:30

Input Set : A:\10\_032221.ST25.txt

Output Set: N:\CRF4\10302002\J032221B.raw

L:47 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:45  
 L:210 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:208  
 L:373 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:371  
 L:1146 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
 L:1323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0